
Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=18; hr=17; min=45; sec=55; ms=198;]

Reviewer Comments:

<210> 3

<211> 30

<212> DNA

<213> Sense primer

<400> 3

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30

The above <213> response is invalid, per 1.823 of the Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown." "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section. Same error in Sequences 4-6.

Validated By CRFValidator v 1.0.3

Application No: 10590034 Version No: 1.0

Input Set:

Output Set:

Started: 2008-03-06 15:23:15.961

Finished: 2008-03-06 15:23:16.241

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 280 ms

Total Warnings: 4

Total Errors: 0

No. of SeqIDs Defined: 6

Actual SeqID Count: 6

Error code		Error Description							
W	402	Undefined organism found in <213> in SEQ ID (3)							
W	402	Undefined organism found in <213> in SEQ ID (4)							
W	402	Undefined organism found in <213> in SEQ ID (5)							
W	402	Undefined organism found in <213> in SEQ ID (6)							

SEQUENCE LISTING

<110>	Genomine, Inc. Korea Research Institute of Chemical Technology	
<120>	Polypeptide Participating in Pyridoxine Biosynthesis, a Polynucleotide Coding the Polypeptide and Those Uses	
<130>	DJKIM.GENO.PT1	
<140>		
	2008-03-06	
	PCT/KR05/000453 2006-08-18	
<150>	PCT/KR2005/000453	
<151>	2005-02-18	
<150> <151>	10-2004-0011517 2004-02-20	
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<170>	PatentIn version 3.3	
<210>	1	
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<212>	DNA	
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Leu Arg Gly Gly Val Ile Met Asp Val Val Asn Ala Glu Gln Ala Arg 35 40 45

Ile Ala Glu Glu Ala Gly Ala Cys Ala Val Met Ala Leu Glu Arg Val 50 55 60

Pro Ala Asp Ile Arg Ala Gln Gly Gly Val Ala Arg Met Ser Asp Pro 65 70 75 80

Gln Met Ile Lys Glu Ile Lys Gln Ala Val Thr Ile Pro Val Met Ala 85 90 95

Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Ile Leu Glu Ala Ile 100 105 110

Gly Ile Asp Tyr Ile Asp Glu Ser Glu Val Leu Thr Leu Ala Asp Glu 115 120 125 Asp His His Ile Asn Lys His Asn Phe Arg Ile Pro Phe Val Cys Gly
130 135 140

Met Ile Arg Thr Lys Gly Glu Ala Gly Thr Gly Asn Ile Ile Glu Ala 165 170 175

Val Arg His Val Arg Ser Val Asn Gly Asp Ile Arg Val Leu Arg Asn 180 185 190

Met Asp Asp Asp Glu Val Phe Thr Phe Ala Lys Lys Leu Ala Ala Pro 195 200 205

Tyr Asp Leu Val Met Gln Thr Lys Gln Leu Gly Arg Leu Pro Val Val 210 215 220

Gln Phe Ala Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Met 225 230 235 240

Met Gln Leu Gly Cys Asp Gly Val Phe Val Gly Ser Gly Ile Phe Lys
245 250 255

Ser Gly Asp Pro Ala Arg Arg Ala Arg Ala Ile Val Gln Ala Val Thr 260 265 270

His Tyr Ser Asp Pro Glu Met Leu Val Glu Val Ser Cys Gly Leu Gly 275 280 285

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